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SEQUENCE LISTING

<110> Aventis Pasteur Limited
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 Raudonikiene, Ausra
 Gallichan, Scott
 Murdin, Andrew

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<150> 60/481,690
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Ala Thr Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Ile
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aaa aaa acc cat tac aaa aat atc ccc atc tta tct gga tta tta atg Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met 530 535 540			1632
aga ata gtg gag cga gct cgg tac caa gct tac gta gaa caa aaa ctc Arg Ile Val Glu Arg Ala Arg Tyr Gln Ala Tyr Val Glu Gln Lys Leu 545 550 555 560			1680
atc tca gaa gag gat Ile Ser Glu Glu Asp 565			1695

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 <211> 565
 <212> PRT
 <213> Chlamydia muridarum

Met Cys Asp Phe Pro Pro Ser Val Ser Gln Lys Ile Leu Phe Leu Cys
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 Gln Lys Ser Ile Pro Gln Ala Leu Glu Ser Tyr Leu Glu Ala Ser Thr
 20 25 30
 Thr Tyr Gln Gln His Asn Phe Ser Ile Leu Arg Leu Ile Ala Lys Ser
 35 40 45
 Tyr Leu Gln Gln Ser Leu Phe Ser Glu Asp Ala Tyr Val Arg Lys Ser
 50 55 60
 Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Thr Leu Asp Leu
 65 70 75 80
 Leu Ser Glu Ser Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu Leu Ile
 85 90 95
 Leu Asn Ala Ala Gly Asn Gln Leu Gly Lys Thr Ser Asp Arg Leu Leu
 100 105 110
 Phe Lys Gly Leu Thr Ala Pro His Pro Ile Ile Arg Leu Glu Ala Ala
 115 120 125
 Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr Leu Tyr
 130 135 140
 Ser Phe Ile His Gln Leu Pro Glu Glu Ile Gln Asn Leu Ala Ala Thr
 145 150 155 160
 Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Val His Arg
 165 170 175
 Leu Leu Ser Ser Pro Asn Ser Leu Thr Arg Asn Tyr Met Ala Tyr Leu
 180 185 190
 Ile Gly Glu Tyr Gln Gln Arg Arg Phe Leu Pro Thr Leu Arg Ser Leu
 195 200 205
 Leu Thr Ser Ala Ala Pro Leu Asp Gln Glu Gly Ser Leu Tyr Ala Ile
 210 215 220

Gly Lys Leu Glu Asp Ala Ser Ser Tyr Pro Lys Ile Lys Ala Leu Ser
 225 230 235 240
 Ser Lys Ser Asn Pro Glu Val Ala Leu Ala Ala Ala Gln Thr Leu Leu
 245 250 255
 Phe Leu Gly Lys Glu Asp Glu Ala Leu Pro Ile Leu Thr Thr Phe Cys
 260 265 270
 Gln Gln Glu Leu Pro Arg Ala Ile Tyr Thr Ser Arg Phe Leu Ser Leu
 275 280 285
 Glu Lys Gly Glu Glu Leu Leu Leu Pro Ile Phe Cys Lys Ala Ile Lys
 290 295 300
 Glu Glu Ile Lys Leu Asn Ala Ala Leu Ala Leu Val His Leu Gly Ser
 305 310 315 320
 Val Asn His Leu Val Leu Ser Tyr Leu Thr Glu Phe Leu Glu Asn Lys
 325 330 335
 Ile Leu His Arg Ile Phe Leu Pro Thr His Ser Ile Gly Lys Ala Thr
 340 345 350
 Gln Phe Trp Lys Glu Cys Thr Ala Leu Pro Leu Leu Ser Pro Glu Glu
 355 360 365
 Lys Ala Arg Ala Leu Ala Met Tyr Arg Ala Ala Glu Asp Thr Ile Leu
 370 375 380
 Ser Ser Leu Leu Lys Leu Pro Asn Asn Ala Tyr Leu Pro Tyr Leu Glu
 385 390 395 400
 Arg Ile Leu Thr Ser Gln Lys Thr Pro Leu Ala Ala Lys Ala Ile Ala
 405 410 415
 Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val Ser Lys
 420 425 430
 Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala Asn Leu
 435 440 445

Ala Leu Tyr Thr Met Thr Gln Asp Pro Glu Lys Lys Ala Leu Leu Tyr
 450 455 460

Gln Tyr Ala Glu Gln Leu Ile Gly Asp Thr Ile Leu Phe Thr Asp Glu
 465 470 475 480

Glu Asn Pro Leu Pro Ser Pro His Ser Ser Tyr Leu Arg Tyr Gln Val
 485 490 495

Ser Pro Glu Thr Arg Ser Gln Leu Met Leu Thr Ile Leu Glu Thr Leu
 500 505 510

Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met
 515 520 525

Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met
 530 535 540

Arg Ile Val Glu Arg Ala Arg Tyr Gln Ala Tyr Val Glu Gln Lys Leu
 545 550 555 560

Ile Ser Glu Glu Asp
 565

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 <211> 1644
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 <213> Chlamydia trachomatis

<220>
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 1 5 10 15
 cga aaa tca gtc cct caa gct cta gaa gcc tat ctc gaa gct tca gca 96
 Arg Lys Ser Val Pro Gln Ala Leu Glu Ala Tyr Leu Glu Ala Ser Ala
 20 25 30
 act tat caa caa cac gat ttc tcc gta tta cgc gta ata gca gaa tcg 144
 Thr Tyr Gln Gln His Asp Phe Ser Val Leu Arg Val Ile Ala Glu Ser
 35 40 45

Tyr	Leu	Gln	Gln	Ser	Phe	Leu	Ser	Glu	Asp	Thr	Tyr	Ile	Arg	Lys	Ser	
50						55					60					
gca	att	att	gga	gca	ggg	cta	tct	ggt	tca	tca	gaa	gct	tta	gag	tta	240
Ala	Ile	Ile	Gly	Ala	Gly	Leu	Ser	Gly	Ser	Ser	Glu	Ala	Leu	Glu	Leu	
65					70				75					80		
ctg	tct	gag	gct	ata	gaa	acg	caa	gat	ctc	tat	gag	caa	cta	ctc	att	288
Leu	Ser	Glu	Ala	Ile	Glu	Thr	Gln	Asp	Leu	Tyr	Glu	Gln	Leu	Leu	Ile	
				85				90					95			
tta	aat	gct	gca	acc	agc	caa	tta	agc	aaa	act	tct	gac	aaa	ctt	tta	336
Leu	Asn	Ala	Ala	Thr	Ser	Gln	Leu	Ser	Lys	Thr	Ser	Asp	Lys	Leu	Leu	
			100					105					110			
ttc	aag	gga	tta	aca	gct	tct	cat	cct	gtc	atc	cgc	tta	gaa	gct	gct	384
Phe	Lys	Gly	Leu	Thr	Ala	Ser	His	Pro	Val	Ile	Arg	Leu	Glu	Ala	Ala	
		115					120					125				
tat	cgt	ctt	gcc	tgt	atg	aaa	aat	agc	aag	gta	agt	gat	tac	ctt	tat	432
Tyr	Arg	Leu	Ala	Cys	Met	Lys	Asn	Ser	Lys	Val	Ser	Asp	Tyr	Leu	Tyr	
	130					135					140					
tct	ttt	atc	tac	aag	tta	cca	gaa	gaa	att	caa	aac	cta	gcg	gca	act	480
Ser	Phe	Ile	Tyr	Lys	Leu	Pro	Glu	Glu	Ile	Gln	Asn	Leu	Ala	Ala	Thr	
145					150					155					160	
att	ttc	tta	caa	ctc	gaa	aca	gaa	gaa	gct	gat	gct	tat	att	cat	cat	528
Ile	Phe	Leu	Gln	Leu	Glu	Thr	Glu	Glu	Ala	Asp	Ala	Tyr	Ile	His	His	
				165					170					175		
ttg	ctc	tct	tct	ccc	aat	aac	ctg	aca	aga	aac	tat	gtt	gcc	tat	tta	576
Leu	Leu	Ser	Ser	Pro	Asn	Asn	Leu	Thr	Arg	Asn	Tyr	Val	Ala	Tyr	Leu	
			180					185					190			
att	gga	gag	tac	aaa	caa	aaa	aga	ttt	ctt	cca	aca	cta	cgc	tct	tta	624
Ile	Gly	Glu	Tyr	Lys	Gln	Lys	Arg	Phe	Leu	Pro	Thr	Leu	Arg	Ser	Leu	
		195					200					205				
ctt	aca	agt	gcc	tct	cct	tta	gat	caa	gaa	ggc	gct	ttg	tat	gcg	tta	672
Leu	Thr	Ser	Ala	Ser	Pro	Leu	Asp	Gln	Glu	Gly	Ala	Leu	Tyr	Ala	Leu	
	210					215					220					
ggc	aaa	ctg	gaa	gac	tct	ggt	agc	tat	cct	aga	att	aaa	gct	cta	agc	720
Gly	Lys	Leu	Glu	Asp	Ser	Gly	Ser	Tyr	Pro	Arg	Ile	Lys	Ala	Leu	Ser	
225					230					235				240		
tct	aga	tcc	aat	cct	gaa	gta	gta	ctc	gct	gca	gct	cag	aca	tta	tta	768
Ser	Arg	Ser	Asn	Pro	Glu	Val	Val	Leu	Ala	Ala	Ala	Gln	Thr	Leu	Leu	
				245					250					255		
ttc	tta	gag	aaa	gaa	gaa	gaa	gct	cta	ccg	atc	cta	acc	aac	ctt	tgc	816
Phe	Leu	Glu	Lys	Glu	Glu	Glu	Ala	Leu	Pro	Ile	Leu	Thr	Asn	Leu	Cys	
			260					265					270			
caa	caa	aaa	ctt	ctt	cga	gcc	ctg	tat	acc	gca	cgt	ttc	ctc	tcg	caa	864

275	280	285	
gag aag ggt gaa gag ctt ctt ctt cca atc ttt tat aac gca aca caa			912
Glu Lys Gly Glu Glu Leu Leu Leu Pro Ile Phe Tyr Asn Ala Thr Gln			
290	295	300	
gaa gaa att aga ctg aat act gct tta gca ctt gtt cat caa ggg tgt			960
Glu Glu Ile Arg Leu Asn Thr Ala Leu Ala Leu Val His Gln Gly Cys			
305	310	315	320
aca gat cct caa gtc ctc cac tat cta aca gaa atc tta gaa agt aaa			1008
Thr Asp Pro Gln Val Leu His Tyr Leu Thr Glu Ile Leu Glu Ser Lys			
	325	330	335
gtt ctc cat cgc ata ttt tta cct act cac tcg aca gga aaa gct ata			1056
Val Leu His Arg Ile Phe Leu Pro Thr His Ser Thr Gly Lys Ala Ile			
	340	345	350
cag ttc tgg aaa gaa tgc acc act ttt cct ctc atg agc caa gaa gac			1104
Gln Phe Trp Lys Glu Cys Thr Thr Phe Pro Leu Met Ser Gln Glu Asp			
	355	360	365
aaa atg aga acg ttg gct atg tat cgg gta gcg gaa gat acc atc ctc			1152
Lys Met Arg Thr Leu Ala Met Tyr Arg Val Ala Glu Asp Thr Ile Leu			
	370	375	380
tca gcg tta cta aaa tta ccc aat gac gcc tat ctt cct tac cta gag			1200
Ser Ala Leu Leu Lys Leu Pro Asn Asp Ala Tyr Leu Pro Tyr Leu Glu			
	385	390	400
cgc atc ctc gcc tca caa aaa act ata cta gca gct aaa gct att gct			1248
Arg Ile Leu Ala Ser Gln Lys Thr Ile Leu Ala Ala Lys Ala Ile Ala			
	405	410	415
ttt tta tcg gta aca gct cat cct cag gca ctt tct tta gtc tcg aaa			1296
Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val Ser Lys			
	420	425	430
gct gca tta act cct gga gac cct atc att cgc gct tac gct aat cta			1344
Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala Asn Leu			
	435	440	445
gct tta tat aca atg acc aaa gat cct gag aaa aaa gct gtg cta tac			1392
Ala Leu Tyr Thr Met Thr Lys Asp Pro Glu Lys Lys Ala Val Leu Tyr			
	450	455	460
cga tat gct gaa caa tta ata gag gat acc att tta ttc aca gat gct			1440
Arg Tyr Ala Glu Gln Leu Ile Glu Asp Thr Ile Leu Phe Thr Asp Ala			
	465	470	480
gaa aat ccg ctt ccc tct cca agc tct tct tat tta cgc tac caa gta			1488
Glu Asn Pro Leu Pro Ser Pro Ser Ser Tyr Leu Arg Tyr Gln Val			
	485	490	495
tcc cct gag acc cgc aca caa ctt atg cta gct att ttg gaa acc tta			1536
Ser Pro Glu Thr Arg Thr Gln Leu Met Leu Ala Ile Leu Glu Thr Leu			

gtt tct tcc aaa acg gat gaa gat atc cgc gtt ttt ctt tcc cta atg 1584
 Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met
 515 520 525

aaa aaa acc cat tac aaa aat atc ccg atc tta tca gga ttg tta atg 1632
 Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met
 530 535 540

aga ata gtg gag 1644
 Arg Ile Val Glu
 545

<210> 8
 <211> 548
 <212> PRT
 <213> Chlamydia trachomatis

<400> 8

Met Cys Asp Phe Pro Ser Ser Val Ser Gln Arg Ile Leu Phe Ser Cys
 1 5 10 15

Arg Lys Ser Val Pro Gln Ala Leu Glu Ala Tyr Leu Glu Ala Ser Ala
 20 25 30

Thr Tyr Gln Gln His Asp Phe Ser Val Leu Arg Val Ile Ala Glu Ser
 35 40 45

Tyr Leu Gln Gln Ser Phe Leu Ser Glu Asp Thr Tyr Ile Arg Lys Ser
 50 55 60

Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Ala Leu Glu Leu
 65 70 75 80

Leu Ser Glu Ala Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu Leu Ile
 85 90 95

Leu Asn Ala Ala Thr Ser Gln Leu Ser Lys Thr Ser Asp Lys Leu Leu
 100 105 110

Phe Lys Gly Leu Thr Ala Ser His Pro Val Ile Arg Leu Glu Ala Ala
 115 120 125

Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr Leu Tyr
 130 135 140

Ser Phe Ile Tyr Lys Leu Pro Glu Glu Ile Gln Asn Leu Ala Ala Thr
 145 150 155 160
 Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Ile His His
 165 170 175
 Leu Leu Ser Ser Pro Asn Asn Leu Thr Arg Asn Tyr Val Ala Tyr Leu
 180 185 190
 Ile Gly Glu Tyr Lys Gln Lys Arg Phe Leu Pro Thr Leu Arg Ser Leu
 195 200 205
 Leu Thr Ser Ala Ser Pro Leu Asp Gln Glu Gly Ala Leu Tyr Ala Leu
 210 215 220
 Gly Lys Leu Glu Asp Ser Gly Ser Tyr Pro Arg Ile Lys Ala Leu Ser
 225 230 235 240
 Ser Arg Ser Asn Pro Glu Val Val Leu Ala Ala Ala Gln Thr Leu Leu
 245 250 255
 Phe Leu Glu Lys Glu Glu Glu Ala Leu Pro Ile Leu Thr Asn Leu Cys
 260 265 270
 Gln Gln Lys Leu Leu Arg Ala Leu Tyr Thr Ala Arg Phe Leu Ser Gln
 275 280 285
 Glu Lys Gly Glu Glu Leu Leu Leu Pro Ile Phe Tyr Asn Ala Thr Gln
 290 295 300
 Glu Glu Ile Arg Leu Asn Thr Ala Leu Ala Leu Val His Gln Gly Cys
 305 310 315 320
 Thr Asp Pro Gln Val Leu His Tyr Leu Thr Glu Ile Leu Glu Ser Lys
 325 330 335
 Val Leu His Arg Ile Phe Leu Pro Thr His Ser Thr Gly Lys Ala Ile
 340 345 350
 Gln Phe Trp Lys Glu Cys Thr Thr Phe Pro Leu Met Ser Gln Glu Asp
 355 360 365

370 375 380
 Ser Ala Leu Leu Lys Leu Pro Asn Asp Ala Tyr Leu Pro Tyr Leu Glu
 385 390 395 400
 Arg Ile Leu Ala Ser Gln Lys Thr Ile Leu Ala Ala Lys Ala Ile Ala
 405 410 415
 Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val Ser Lys
 420 425 430
 Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala Asn Leu
 435 440 445
 Ala Leu Tyr Thr Met Thr Lys Asp Pro Glu Lys Lys Ala Val Leu Tyr
 450 455 460
 Arg Tyr Ala Glu Gln Leu Ile Glu Asp Thr Ile Leu Phe Thr Asp Ala
 465 470 475 480
 Glu Asn Pro Leu Pro Ser Pro Ser Ser Ser Tyr Leu Arg Tyr Gln Val
 485 490 495
 Ser Pro Glu Thr Arg Thr Gln Leu Met Leu Ala Ile Leu Glu Thr Leu
 500 505 510
 Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met
 515 520 525
 Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met
 530 535 540
 Arg Ile Val Glu
 545

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 <213> Chlamydia trachomatis

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41

<210> 10
<211> 40
<212> DNA
<213> Chlamydia trachomatis

<400> 10
gttggtaccg agctcgctcc actattctca ttaataatcc

40

<210> 11
<211> 41
<212> DNA
<213> Chlamydia trachomatis

<400> 11
ataagaatgc ggccgccacc atgtgcgact tccccccag t

41

<210> 12
<211> 40
<212> DNA
<213> Chlamydia trachomatis

<400> 12
gttggtaccg agctcgctcc actattctca ttaataatcc

40

<210> 13
<211> 31
<212> DNA
<213> Chlamydia trachomatis

<400> 13
gaattcggat ccgatgggat tatctgcct a

31

<210> 14
<211> 36
<212> DNA
<213> Chlamydia trachomatis

<400> 14
attaagaatg cggccgcttt atcactccac tattct

36